

0905

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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/783,320

DATE: 09/10/2001  
 TIME: 11:21:51

Input Set : A:\LEX-0137-USA SEQLIST.txt  
 Output Set: N:\CRF3\09102001\I783320.raw

4 <110> APPLICANT: Walke, D. Wade  
 5       Hu, Yi  
 6       Nepomichy, Boris  
 7       Turner, C. Alexander Jr  
 8       Zambrowicz, Brian  
 11 <120> TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same  
 13 <130> FILE REFERENCE: LEX-0137-USA  
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/783,320  
 C--> 15 <141> CURRENT FILING DATE: 2001-02-15  
 15 <150> PRIOR APPLICATION NUMBER: US 60/183,582  
 16 <151> PRIOR FILING DATE: 2000-02-18  
 18 <150> PRIOR APPLICATION NUMBER: US 60/184,014  
 19 <151> PRIOR FILING DATE: 2000-02-22  
 21 <160> NUMBER OF SEQ ID NOS: 50  
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 3108  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: homo sapiens  
 30 <400> SEQUENCE: 1

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32	tcctatgatc	tccgcagttt	ggtgtctcag	ttatttaaaa	gaaatccat	ggatagacca	120
33	tcagtcaact	ccatattgga	gaaaggtttt	atagccaaac	gcattgaaaa	gtttctct	180
34	cctcagctta	ttgcagaaga	attttgtcta	aaaacatttt	cgaagtttgg	atcacagcct	240
35	ataccagcta	aaagaccagc	tccaggacaa	aactcgattt	ctgttatgcc	tgctcagaaaa	300
36	attacaaagc	ctgcccctaa	atatgaaata	cccttagcat	ataagaata	tggagataaaa	360
37	aaattacacg	aaaagaaaacc	actgcaaaaaa	cataaacagg	cccatcaaac	tccagagaag	420
38	agagtgaata	ctggagaaga	aaggaggaaa	atatctgagg	aagcagcaag	aaagagaagg	480
39	ctgaaattta	ttgaaaaaaa	aaagaaacaa	aaggatcaga	ttatttagttt	aatgaaggct	540
40	gaacaaatga	aaaggcaaga	aaaggaaagg	ttggaaagaa	taaatagggc	cagggAACAA	600
41	ggatggagaa	atgtgctaag	tgctggtgg	agtggtgaag	taaaggctcc	ttttctggc	660
42	agtggaggg	ctatagctcc	atcatcttt	tcttctcgag	gacagtatga	acattaccat	720
43	gccatttttg	accaaatgca	gcaacaaaga	gcagaagata	atgaagctaa	atggaaaaga	780
44	gaardatatg	gtcgaggct	tccagaaagg	caaaaaggc	agctagctgt	agaaagagct	840
45	aaacaagtag	aagagttct	gcagcggaaa	cggaaagcta	tgcagaataa	agctcgagcc	900
46	gaaggacata	tggaaatcct	gcaaaacctg	gcagctatgt	atggaggcag	gcccaagctct	960
47	tcaagaggag	ggaagccaa	aaacaaagag	gaagaggttt	atctggcaag	actgaggcaa	1020
48	ataagactac	agaatttcaa	tgagcgc	cagattaaag	ccaaacttcg	tggtaaaaag	1080
49	aaagaagcta	atcattctga	aggacaagaa	ggaagtgaag	aggctgcacat	gaggcgc	1140
50	aaaatcgat	cactgaaggc	ccatgcaat	gcacgtctg	ctgtactaaa	agaacaacta	1200
51	gaacgaaaga	gaaaggagc	ttatgagaga	gaaaaaaaaa	tgtggaaaga	gcatttgg	1260
52	gctaaaggag	ttaagagttc	tgatgttct	ccacctttgg	gacagcatga	aacaggtggc	1320
53	tctccatcaa	agcaacagat	gagatctgtt	atttctgtaa	cttcagcttt	gaaagaagtt	1380
54	ggcgtggaca	gtagtttaac	tgatacccg	gaaacttcag	aagagatgca	aaagaccaac	1440
55	aatgcttattt	caagtaagcg	agaaatactt	cgcagattaa	atgaaaatct	taaagctcaa	1500
56	gaagatgaaa	aaggaatgca	gaatctct	gatactttt	agataaaatgt	tcatgaagat	1560
57	gccaagagc	atgaaaaaaa	aaaatcagtt	tcatctgatc	gcaagaatgt	ggaggcagga	1620

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58	ggtaacttg	tgattcctct	ggatgagtt	acactagata	catccttctc	tacaactgaa	1680
59	agacatacag	tggagaagt	tattaaatta	ggtcataatg	gatctccaag	aagagcctgg	1740
60	gggaaaagtc	cgacagattc	tgttctaaag	atacttggag	aagctgaact	acaacttcag	1800
61	acagaactat	tagaaaatac	aactattaga	agttagattt	ctcccaagg	ggaaaagtac	1860
62	aaacccttaa	ttactggaga	aaaaaaaagta	caatgtat	cacatgaaat	aaacccatca	1920
63	gctattgtt	atttcctgt	tgagacaaaa	agtcccgagt	tcagtggagc	atctccacag	1980
64	atgtcattga	aactggaagg	aaatttagaa	gaacctgat	atggaaac	agaaattcta	2040
65	caagagccaa	gtgaaacaaa	caaagatgag	agcttgcac	gcactattac	tgatgtgtgg	2100
66	attagtgagg	aaaaagaaaac	aaaggaaact	cagtccgcag	ataggatcac	cattcaggaa	2160
67	aatgaagttt	ctgaagatgg	agtctcgagt	actgtggacc	aacttagtga	cattcatata	2220
68	gaggctggaa	ccatgatc	tcagcactct	aaatgtgat	tagataagtc	tgtcaaccg	2280
69	gaaccat	tccataaggt	ggttcattct	gaacacttga	acttagtccc	tcaagtcaa	2340
70	tcagttcagt	gttcaccaga	agaatcctt	gcatttcgat	ctcactcgca	tttaccacca	2400
71	aaaaataaaa	acaagaattc	cttgcgtatt	ggacttcaa	ctggctgtt	tgatgcaaac	2460
72	aacccaaaga	tgttaaggac	atgttca	ccagatctct	caaagctgtt	cagaaccctt	2520
73	atggatgtt	ccaccgtagg	agatgtcgt	caagacaatc	ttgaaataga	tgaaattaaa	2580
74	gataaaaaca	ttaaagaagg	accttctgat	tctgaagaca	ttgtgttga	agaaactgac	2640
75	acagatttac	aagagctgca	ggcctcgat	gaacagttac	ttagggaaaca	acctggtaa	2700
76	gaatacagt	aagaagaaga	gtcagtctt	aagaacagtg	atgtggagcc	aactgcaa	2760
77	gggacagatg	tggcagatga	agatgacaat	cccagtagtg	aaagtgcct	gaacgaagaa	2820
78	tggcactcag	ataacagt	tgttggaaatt	gctgtgaat	gtgaatgcg	tagtgtctt	2880
79	aaccatttag	aggaactgag	acttcatct	gagcaggaaa	ttggcttga	aaaattctt	2940
80	gaggtttatg	agaaaataaa	ggctattcat	gaagatgaag	atggaaat	tgaaattttgt	3000
81	tcaaaaatag	ttcaaaaat	tttggaaat	gaacatcagc	atcttatgc	caagattctt	3060
82	catttagtca	tggcagatgg	agcctaccaa	gaagataatg	atgaataa		3108

84 <210> SEQ ID NO: 2

85 <211> LENGTH: 1035

86 <212> TYPE: PRT

87 <213> ORGANISM: homo sapiens

88 <400> SEQUENCE: 2

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91	1				5				10					15		
92	Ser	Leu	His	Tyr	Ser	Tyr	Asp	Leu	Arg	Ser	Leu	Val	Ser	Gln	Leu	Phe
93						20			25					30		
94	Lys	Arg	Asn	Pro	Arg	Asp	Arg	Pro	Ser	Val	Asn	Ser	Ile	Leu	Glu	Lys
95						35			40					45		
96	Gly	Phe	Ile	Ala	Lys	Arg	Ile	Glu	Lys	Phe	Leu	Ser	Pro	Gln	Leu	Ile
97						50			55					60		
98	Ala	Glu	Glu	Phe	Cys	Leu	Lys	Thr	Phe	Ser	Lys	Phe	Gly	Ser	Gln	Pro
99						65			70					75		80
100	Ile	Pro	Ala	Lys	Arg	Pro	Ala	Ser	Gly	Gln	Asn	Ser	Ile	Ser	Val	Met
101						85			90					95		
102	Pro	Ala	Gln	Lys	Ile	Thr	Lys	Pro	Ala	Ala	Lys	Tyr	Gly	Ile	Pro	Leu
103						100			105					110		
104	Ala	Tyr	Lys	Lys	Tyr	Gly	Asp	Lys	Lys	Leu	His	Glu	Lys	Lys	Pro	Leu
105						115			120					125		
106	Gln	Lys	His	Lys	Gln	Ala	His	Gln	Thr	Pro	Glu	Lys	Arg	Val	Asn	Thr
107						130			135					140		
108	Gly	Glu	Glu	Arg	Arg	Lys	Ile	Ser	Glu	Glu	Ala	Ala	Arg	Lys	Arg	Arg

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109	145	150	155	160												
110	Leu	Glu	Phe	Ile	Glu	Lys	Glu	Lys	Lys	Gln	Lys	Asp	Gln	Ile	Ile	Ser
111																
112	Leu	Met	Lys	Ala	Glu	Gln	Met	Lys	Arg	Gln	Glu	Lys	Glu	Arg	Leu	Glu
113																
114	Arg	Ile	Asn	Arg	Ala	Arg	Glu	Gln	Gly	Trp	Arg	Asn	Val	Leu	Ser	Ala
115																
116	Gly	Gly	Ser	Gly	Glu	Val	Lys	Ala	Pro	Phe	Leu	Gly	Ser	Gly	Gly	Thr
117																
118	Ile	Ala	Pro	Ser	Ser	Phe	Ser	Ser	Arg	Gly	Gln	Tyr	Glu	His	Tyr	His
119																
120	Ala	Ile	Phe	Asp	Gln	Met	Gln	Gln	Gln	Arg	Ala	Glu	Asp	Asn	Glu	Ala
121																
122	Lys	Trp	Lys	Arg	Glu	Ile	Tyr	Gly	Arg	Gly	Leu	Pro	Glu	Arg	Gln	Lys
123																
124	Gly	Gln	Leu	Ala	Val	Glu	Arg	Ala	Lys	Gln	Val	Glu	Glu	Phe	Leu	Gln
125																
126	Arg	Lys	Arg	Glu	Ala	Met	Gln	Asn	Lys	Ala	Arg	Ala	Glu	Gly	His	Met
127																
128	Gly	Ile	Leu	Gln	Asn	Leu	Ala	Ala	Met	Tyr	Gly	Gly	Arg	Pro	Ser	Ser
129																
130	Ser	Arg	Gly	Gly	Lys	Pro	Arg	Asn	Lys	Glu	Glu	Glu	Val	Tyr	Leu	Ala
131																
132	Arg	Leu	Arg	Gln	Ile	Arg	Leu	Gln	Asn	Phe	Asn	Glu	Arg	Gln	Gln	Ile
133																
134	Lys	Ala	Lys	Leu	Arg	Gly	Glu	Lys	Lys	Glu	Ala	Asn	His	Ser	Glu	Gly
135																
136	Gln	Glu	Gly	Ser	Glu	Glu	Ala	Asp	Met	Arg	Arg	Lys	Lys	Ile	Glu	Ser
137																
138	Leu	Lys	Ala	His	Ala	Asn	Ala	Arg	Ala	Ala	Val	Leu	Lys	Glu	Gln	Leu
139																
140	Glu	Arg	Lys	Arg	Lys	Glu	Ala	Tyr	Glu	Arg	Glu	Lys	Lys	Val	Trp	Glu
141																
142	Glu	His	Leu	Val	Ala	Lys	Gly	Val	Lys	Ser	Ser	Asp	Val	Ser	Pro	Pro
143																
144	Leu	Gly	Gln	His	Glu	Thr	Gly	Gly	Ser	Pro	Ser	Lys	Gln	Gln	Met	Arg
145																
146	Ser	Val	Ile	Ser	Val	Thr	Ser	Ala	Leu	Lys	Glu	Val	Gly	Val	Asp	Ser
147																
148	Ser	Leu	Thr	Asp	Thr	Arg	Glu	Thr	Ser	Glu	Glu	Met	Gln	Lys	Thr	Asn
149																
150	Asn	Ala	Ile	Ser	Ser	Lys	Arg	Glu	Ile	Leu	Arg	Arg	Leu	Asn	Glu	Asn
151																
152	Leu	Lys	Ala	Gln	Glu	Asp	Glu	Lys	Gly	Met	Gln	Asn	Leu	Ser	Asp	Thr
153																
154	Phe	Glu	Ile	Asn	Val	His	Glu	Asp	Ala	Lys	Glu	His	Glu	Lys	Glu	Lys
155																
156	Ser	Val	Ser	Ser	Asp	Arg	Lys	Lys	Trp	Glu	Ala	Gly	Gly	Gln	Leu	Val
157																

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158 Ile Pro Leu Asp Glu Leu Thr Leu Asp Thr Ser Phe Ser Thr Thr Glu  
159 545 550 555 560  
160 Arg His Thr Val Gly Glu Val Ile Lys Leu Gly Pro Asn Gly Ser Pro  
161 565 570 575  
162 Arg Arg Ala Trp Gly Lys Ser Pro Thr Asp Ser Val Leu Lys Ile Leu  
163 580 585 590  
164 Gly Glu Ala Glu Leu Gln Leu Gln Thr Glu Leu Leu Glu Asn Thr Thr  
165 595 600 605  
166 Ile Arg Ser Glu Ile Ser Pro Glu Gly Glu Lys Tyr Lys Pro Leu Ile  
167 610 615 620  
168 Thr Gly Glu Lys Lys Val Gln Cys Ile Ser His Glu Ile Asn Pro Ser  
169 625 630 635 640  
170 Ala Ile Val Asp Ser Pro Val Glu Thr Lys Ser Pro Glu Phe Ser Glu  
171 645 650 655  
172 Ala Ser Pro Gln Met Ser Leu Lys Leu Glu Gly Asn Leu Glu Glu Pro  
173 660 665 670  
174 Asp Asp Leu Glu Thr Glu Ile Leu Gln Glu Pro Ser Gly Thr Asn Lys  
175 675 680 685  
176 Asp Glu Ser Leu Pro Cys Thr Ile Thr Asp Val Trp Ile Ser Glu Glu  
177 690 695 700  
178 Lys Glu Thr Lys Glu Thr Gln Ser Ala Asp Arg Ile Thr Ile Gln Glu  
179 705 710 715 720  
180 Asn Glu Val Ser Glu Asp Gly Val Ser Ser Thr Val Asp Gln Leu Ser  
181 725 730 735  
182 Asp Ile His Ile Glu Pro Gly Thr Asn Asp Ser Gln His Ser Lys Cys  
183 740 745 750  
184 Asp Val Asp Lys Ser Val Gln Pro Glu Pro Phe Phe His Lys Val Val  
185 755 760 765  
186 His Ser Glu His Leu Asn Leu Val Pro Gln Val Gln Ser Val Gln Cys  
187 770 775 780  
188 Ser Pro Glu Glu Ser Phe Ala Phe Arg Ser His Ser His Leu Pro Pro  
189 785 790 795 800  
190 Lys Asn Lys Asn Lys Asn Ser Leu Leu Ile Gly Leu Ser Thr Gly Leu  
191 805 810 815  
192 Phe Asp Ala Asn Asn Pro Lys Met Leu Arg Thr Cys Ser Leu Pro Asp  
193 820 825 830  
194 Leu Ser Lys Leu Phe Arg Thr Leu Met Asp Val Pro Thr Val Gly Asp  
195 835 840 845  
196 Val Arg Gln Asp Asn Leu Glu Ile Asp Glu Ile Lys Asp Glu Asn Ile  
197 850 855 860  
198 Lys Glu Gly Pro Ser Asp Ser Glu Asp Ile Val Phe Glu Glu Thr Asp  
199 865 870 875 880  
200 Thr Asp Leu Gln Glu Leu Gln Ala Ser Met Glu Gln Leu Leu Arg Glu  
201 885 890 895  
202 Gln Pro Gly Glu Glu Tyr Ser Glu Glu Glu Ser Val Leu Lys Asn  
203 900 905 910  
204 Ser Asp Val Glu Pro Thr Ala Asn Gly Thr Asp Val Ala Asp Glu Asp  
205 915 920 925  
206 Asp Asn Pro Ser Ser Glu Ser Ala Leu Asn Glu Glu Trp His Ser Asp

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207 930 935 940  
 208 Asn Ser Asp Gly Glu Ile Ala Ser Glu Cys Glu Cys Asp Ser Val Phe  
 209 945 950 955 960  
 210 Asn His Leu Glu Glu Leu Arg Leu His Leu Glu Gln Glu Met Gly Phe  
 211 965 970 975  
 212 Glu Lys Phe Phe Glu Val Tyr Glu Lys Ile Lys Ala Ile His Glu Asp  
 213 980 985 990  
 214 Glu Asp Glu Asn Ile Glu Ile Cys Ser Lys Ile Val Gln Asn Ile Leu  
 215 995 1000 1005  
 216 Gly Asn Glu His Gln His Leu Tyr Ala Lys Ile Leu His Leu Val Met  
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 218 Ala Asp Gly Ala Tyr Gln Glu Asp Asn Asp Glu  
 219 1025 1030 1035  
 221 <210> SEQ ID NO: 3  
 222 <211> LENGTH: 3645  
 223 <212> TYPE: DNA  
 224 <213> ORGANISM: homo sapiens  
 226 <400> SEQUENCE: 3  
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 229 tccagtaaag aaagagaaga atcaaggaga gaagttgcag tattggcaaa catgaagcat 180  
 230 ccaaataatttgc tccagttatag agaattttttt gaagaaaatg gctctctta catagtaatg 240  
 231 gattactgtg agggaggggta tctgtttaag cgaataaaatg ctcagaaagg cgttttgtt 300  
 232 caagaggatc agattttggta ctgggttgcagatatgtt tggccctgaa acatgtatcat 360  
 233 gatagaaaaaa ttcttcatcg agacattaaa ttcgcagaaca tatttttaac taaagatgg 420  
 234 acagtacaac ttggagatttt tggatttgc agagttctt atagttactgtt agagttggc 480  
 235 cgaacttgc tagggacccc atactacttg tcacctgaaa tctgtgaaaaa caaaccttac 540  
 236 aataataaaa gtgacatttg ggctctgggg tttgttcctt atgagttgt tacacttaaa 600  
 237 catgttttg aagctggcag tatgaaaaac ctggttactga agataatatc tggatctttt 660  
 238 ccacctgtgt ctgttcattt ttcctatgtt cttccgcgtt tgggtctca gttattttaa 720  
 239 agaaatccctt gggatagacc atcgtcaac tccatattgg agaaagggtt tatagccaaa 780  
 240 cgcattgaaa agtttctctc tcctcagttt attgcagaag aattttgtctt aaaaacattt 840  
 241 tcgaagtttgc gatcacagcc tataccagctt aaaaagaccat cttcaggaca aaactcgatt 900  
 242 tctgttatgc ctgttcagaa aattacaaatg cctggcgtt aatatggaaat accttttgc 960  
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 244 gcccattcaaa ctccagagaa gagatgttgc attggagaag aaaggagaa aatatcttgc 1080  
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 246 attatttagtt taatgaaggc tgaacaaatg aaaaggcaag aaaaaggaaatg gttggaaaga 1200  
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 251 cagctagtcg tagaaagagc taaacaagttt gaccaatgc tgcagcggaaa acggaaatgt 1500  
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 253 agactacaga atttcaatgc ggcacacag attaaagccca aacttcgtgg tggaaagaaaa 1620  
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 255 atcgaatcac tgaaggccca tgccaaatgc cgtgtctgc tactaaaga acaactagaa 1740  
 256 cgaaagagaa aggaggctt tgagagagaa aaaaagttt gggaaagagca tttgtggct 1800  
 257 aaaaqgatgtt aagtttgc tggaaatgc ctttgcac aacatgaaac aggtggctt 1860

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No  
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date